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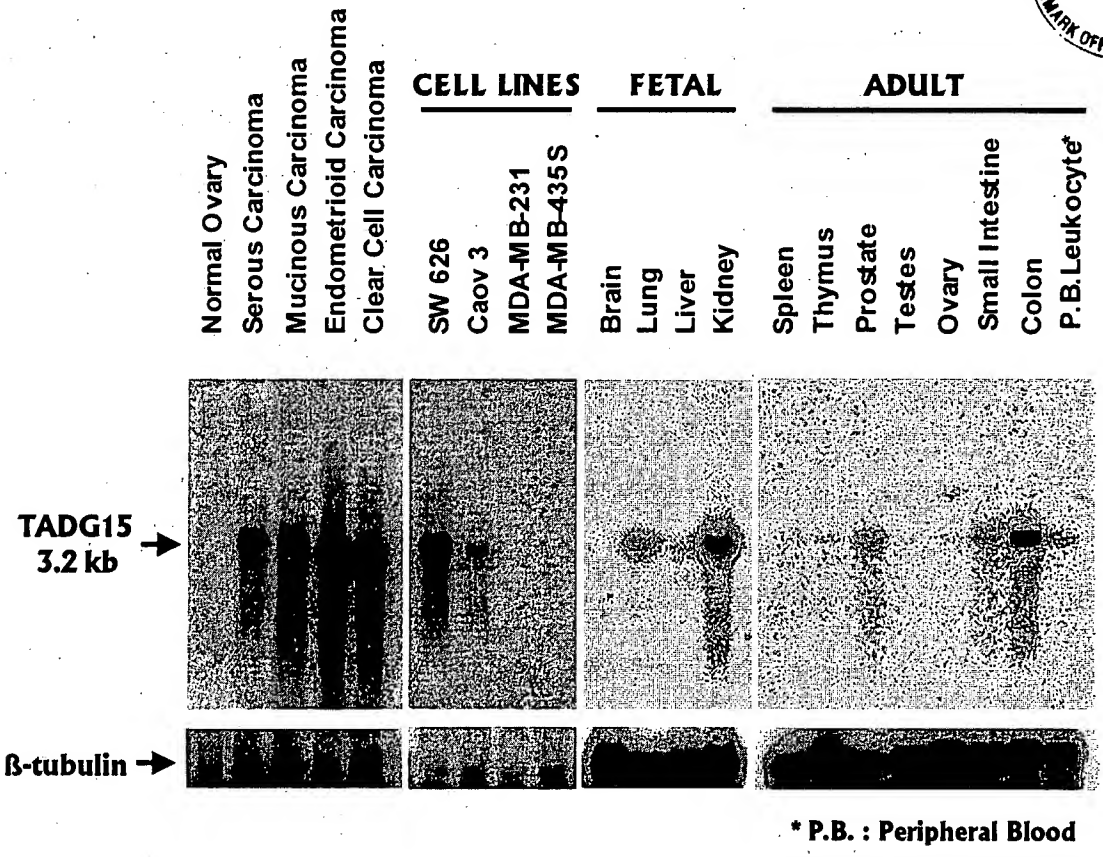

Fig. 5

Fig. 6A

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O.G. FIG.
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Fig. 6B

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O.G. FIG.
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Fig. 7

Fig. 8

Fig. 9

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O.G. FIG.
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Fig. 10A

Fig. 10B

Fig. 10C

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Fig. 10D

Fig. 10E

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```
hTADG15   MGSDRARKGG GGPKDFGAGL KYNSRHEKVN GLEEGVEFLP VNNVKKVEKH  50
mEpithin  ---N-G--A- --SQ------ --D--L-NM- -F-------- A--A-----R

hTADG15   GPGRWVVLAA VLIGLLLVLL GIGFLVWHLQ YRDVRVQKVF NGYMRITNEN 100
mEpithin  --R-----V- --FSF--LS- MA-L----FH --N------- --HL-----I

hTADG15   FVDAYENSNS TEFVSLASKV KDALKLLYSG VPFLGPYHKE SAVTAFSEGS 150
mEpithin  -L------T- ---I----Q- -E------NE --V------K ----------

hTADG15   VIAYYWSEFS IPQHLVEEAE RVMAEERVVM LPPRARSLKS FVVTSVVAFP 200
mEpithin  ---------- --P--A--VD -A--V----T ------A--- --L-------

hTADG15   TDSKTVQRTQ DNSCSFGLHA RGVELMRFTT PGFPDSPYPA HARCQWALRG 250
mEpithin  I-PRML---- ------A--- H-AAVT---- ----N----- ------V---

hTADG15   DADSVLSLTF RSFDLASCDE RGSDLVTVYN TLSPMEPHAL VQLCGTYPPS 300
mEpithin  ---------- ----V-P--- H--------D S--------V -R----FS--

hTADG15   YNLTFHSSQN VLLITLITNT ERRHPGFEAT FFQLPRMSSC GGRLRKAQGT 350
mEpithin  -----L---- -F-V------ G---L----- -----K---- --V-SDT---

hTADG15   FNSPYYPGHY PPNIDCTWNI EVPNNQHVKV SFKFFYLLEP GVPAGTCPKD 400
mEpithin  -S-------- ----N----- K----RN--- R--L---VD- N--V-S-T--

hTADG15   YVEINGEKYC GERSQFVVTS NSNKITVRFH SDQSYTDTGF LAEYLSYDSS 450
mEpithin  --------GS --------S- --S----H-- --H------- ---------N
```

Fig. 11A

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```
hTADG15  DPCPGQFTCR TGRCIRKELR CDGWADCTDH SDELNCSCDA GHQFTCKNKF 500
mEpithin -----M-M-K ---------- -------P-Y ---RY-R-N- T-------Q-

hTADG15  CKPLFWVCDS VNDCGDNSDE QGCSCPAQTF RCSNGKCLSK SQQCNGKDDC 550
mEpithin ---------- ------G--- E------GS- K-------PQ --K-----N-

hTADG15  GDGSDEASCP KVNVVTCTKH TYRCLNGLCL SKGNPECDGK EDCSDGSDEK 600
mEpithin ---------D S----S---Y ----Q----- ---------- T---------

hTADG15  DCDCGLRSFT RQARVVGGTD ADEGEWPWQV SLHALGQGHI CGASLISPNW 650
mEpithin N--------- K--------N ---------- ---------L --------D-

hTADG15  LVSAAHCYID DRGFRYSDPT QWTAFLGLHD QSQRSAPGVQ ERRLKRIISH 700
mEpithin -------FQ- -KN-K---Y- M-------L- --K---S--- -LK-----T-

hTADG15  PFFNDFTFDY DIALLELEKP AEYSSMVRPI CLPDASHVFP AGKAIWVTGW 750
mEpithin -S-------- ---------S V---TV---- -----T---- ----------

hTADG15  GHTQYGGTGA LILQKGEIRV INQTTCENLL PQQITPRMMC VGFLSGGVDS 800
mEpithin ---KE----- ---------- -------D-M ---------- ----------

hTADG15  CQGDSGGPLS SVEADGRIFQ AGVVSWGDGC AQRNKPGVYT RLPLFRDWIK 850
mEpithin ---------- -A-K---M-- -------E-- ---------- ---CSSGLDQ

hTADG15  ENTGV*                                                  900
mEpithin RAHWGIAAWT DSRPQTPTGM PDMHTWIQER NTDDIYAVAS PPQHNPDCEL

hTADG15     SEQ ID NO: 2                                        902
mEpithin HP SEQ ID NO: 10
```

Fig. 11B

APPROVED BY DRAFTSMAN | O.G. FIG. CLASS | SUBCLASS
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TADG15:  TCAAGAGCGGCCTCGGGGTACCATGGGGAGCGATCGGGCCCGCAAGGGCGGAGGGGGCCCGAAGGACTTCGGCGCGGGACT 81

SNC19:   ..............................................................................

 82 CAAGTACAACTCCCGGCACGAGAAAGTGAATGGCTTGGAGGAAGGCGTGGAGTTCCTGCCAGTCAACAACGTCAAGAAGGTGGAAAAGCATGGCCCGGGG

    ..............................................................................

182 CGCTGGGTGGTGCTGGCAGCCGTGCTGATCGGCCTCCTCTTGGTCTTGTTGGGGATCGGCTTCCTGGTGTGGCATTTGCAGTACCGGGACGTGCGTGTCC 281
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  1 CGCTGGGTGGTGCTGGCAGCCGTGCTGATCGGCCTCCTCTTGGTCTTGCTGGGGATCGGCTTCCTGGTGTGGCATTTGCAGTACCGGGACGTGCGTGTCC 100

282 AGAAGGTCTTCAATGGCTACATGAGGATCACAAATGAGAATTTTGTGGATGCCTACGAGAACTCCAACTCCACTGAGTTTGTAAGCCTGGCCAGCAAGGT 381
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
101 AGAAGGTCTTCAATGGCTACATGAGGATCACAAATGAGAATTTTGTGGATGCCTACGAGAACTCCAACTCCACTGAGTTTGTAAGCCTGGCCAGCAAGGT 200

382 GAAGGACGCGCTGAAGCTGCTGTACAGCGGAGTCCCATTCCTGGGCCCCTACCACAAGGAGTCGGCTGTGACGGCCTTCAGCGAGGGCAGCGTCATCGCC 481
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
201 GAAGGACGCGCTGAAGCTGCTGTACAGCGGAGTCCCATTCCTGGGCCCCTACCACAAGGAGTCGGCTGTGACGGCCTTCAGCGAGGGCAGCGTCATCGCC 300

482 TACTACTGGTCTGAGTTCAGCATCCCGCAGCACCTGGTGGAGGAGGCCGAGCGCGTCATGGCCGAGGAGCGCGTAGTCATGCTGCCCCCGCGGGCGCGCT 581
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 TACTACTGGTCTGAGTTCAGCATCCCGCAGCACCTGGTTGAGGAGGCCGAGCGCGTCATGGCC.AGGAGCGCGTAGTCATGCTGCCCCCGCGGGCGCGCT 399

582 CCCTGAAGTCCTTTGTGGTCACCTCAGTGGTGGCTTTCCCCACGGACTCCAAAACAGTACAGACCACCCAGGACAACAGCTGCAGCTTTGGCCTGCACGC 681
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
400 CCCTGAAGTCCTTTGTGGTCACCTCAGTGGTGGCTTTCCCCACGGACTCCAAAACAGTACAGAGGACCCAGGACAACAGCTGCAGCTTTGGCCTGCACG. 498
```

Fig. 12A

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682 CCGCGGTGTGGAGCTGATGCGCTTCACCACGCCCGGCTTCCCTGACAGCCCCTACCCCGCTCATGCCCGCTGCCAGTGGGCCCTGCGGGGGGACGCCGAC 781
    ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
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1375 CCCATGCCCGGGGCAGTTCACGTGCCGCACGGGGCGGTGTATCCGGAAGGAGCTGCGCTGTGATGGCTGGGCCGACTGCACCGACCACAGCGATGAGCTC 1474
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1182 CCCATGCCCGGGGCAGTTCACGTGCCGCACGGGGCGGTGTATCCGGAAGGAGCTGCGCTGTGATGGCTGGG.CGACTGCACCGACCACAGCGATGAGCTC 1290

1475 AACTGCAGTTGCGACGCCGGCCACCAGTTCACGTGCAAGAACAAGTTCTGCAAGCCCCTCTTCTGGGTCTGCGACAGTGTGAACGACTGCGGAGACAACA 1574
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1281 AACTGCAGTTGCGACGCCGGCCACCAGTTCACGTGCAAGAGCAAGTTCTGCAAG...CTCTTCTGGGTCTGCGACAGTGTGAACGAGTGCGGAGACAACA 1377

1575 GCGACGAGCAGGGGTGCAGTTGTCCGG.CCCAGACCTTCAGGTGTTCCAATGGGAAGTGCCTCTCGAAAAGCCAGCAGTGCAATGGGAAGGACGACTGTG 1673
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1378 GCGACGAGCAGGGTTGCATTTGTCCGGACCCAGACCTTCAGGTGTTCCAATGGGAAGTGCCTCTCGAAAAGCCAGCAGTGCAATGGGAAGGACGACTGTG 1477

1674 GGGACGGGTCCGACGAGGCCTCCTGCCCCAAGGTGAACGTCGTCACTTGTACCAAACACACCTACCGCTGCCTCAATGGGCTCTGCTTGAGCAAGGGCAA 1773
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1478 GGGACGGGTCCGACGAGGCCTCCTGCCCCAAGGTGAACGTCGTCACTTGTACCAAACACACCTACCGCTGCCTCAATGGGCTCTGCTTGAGCAAGGGCAA 1577

1774 CCCTGAGTGTGACGGGAAGGAGGACTGTAGCGACGGCTCAGATGAGAAGGACTGCGACTGTGGGCTGCGGTCATTCACGAGACAGGCTCGTGTTGTTGGG 1873
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1578 CCCTGAGTGTGACGGGAAGGAGGACTGTAGCGACGGCTCAGATGAGAAGGACTGCGACTGTGGGCTGCGGTCATTCACGAGACAGGCTCGTGTTGTTGGG 1677

1874 GGCACGGATGCGGATGAGGGCGAGTGGCCCTGGCAGGTAAGCCTGCATGCTCTGGGCCAGGGCCACATCTGCGGTGCTTCCCTCATCTCTCCCAACTGGC 1973
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1678 GGCACGGATGCGGATGAGGGCGAGTGGCCCTGGCAGGTAAGCCTGCATGCTCTGGGCCAGGGCCACATCTGCGGTGCTTCCCTCATCTCTCCCAACTGGC 1777

1974 TGGTCTCTGCCGCACACTGCTACATCGATGACAGAGGATTCAGGTACTCAGACCCCACGCAGTGGACGGCCTTCCTGGGCTTGCACGACCAGAGCCAGCG 2073
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1778 TGGTCTCTGCCGCACACTGCTACATCGATGACAGAGGATTCAGGTACTCAGACCCCACGCA..GGACGGCCTTCCTGGGCTTGCACGACCAGAGCCAGCG 1875
```

Fig. 12C

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2074 CAGCGCCCCTGGGGTGCAGGAGCGCAGGCTCAAGCGCATCATCTCCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATCGCGCTGCTGGAGCTG 2173
     ||  | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1876 CA..GGCCCTGGGGTGCAGGAGCGCAGGCTCAAGCGCATCATCTCCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATCGCGCTGCTGGAGCTG 1973

2174 GAGAAACCGGCAGAGTACAGCTCCATGGTGCGGCCCATCTGCCTGCCGGACGCCTCCCATGTCTTCCCTGCCGGCAAGGCCATCTGGGTCACGGGCTGGG 2273
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
1974 GAGAAACCGGCAGAGTACAGCTCCATGGTGCGGCCCATCTGCCTGCCGGACGCCTGCCATGTCTTCCCTGCCGGCAAGGCCATCTGGGTCACGGGCTGGG 2073

2274 GACACACCCAGTATGGAGGCACTGGCGCGCTGATCCTGCAAAAGGGTGAGATCCGCGTCATCAACCAGACCACCTGCGAGAACCTCCTGCCGCAGCAGAT 2373
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2074 GACACACCCAGTATGGAGGCACTGGCGCGCTGATCCTGCAAAAGGGTGAGATCCGCGTCATCAACCAGACCACCTGCGAGAACCTCCTGCCGCAGCAGAT 2173

2374 CACGCCGCGCATGATGTGCGTGGGCTTCCTCAGCGGCGGCGTGGACTCCTGCCAGGGTGATTCCGGGGGACCCCTGTCCAGCGTGGAGGCGGATGGGCGG 2473
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2174 CACGCCGCGCATGATGTGCGTGGGCTTCCTCAGCGGCGGCGTGGACTCCTGCCAGGGTGATTCCGGGGGACCCCTGTCCAGCGTGGAGGCGGATGGGCGG 2273

2474 ATCTTCCAGGCCGGTGTGGTGAGCTGGGGAGACGGCTGCGCTCAGAGGAACAAGCCAGGCGTGTACACAAGGCTCCCTCTGTTTCGGGACTGGATCAAAG 2573
     |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
2274 ATCTTCCAGGCCGGTGTGGTGAGCTGGGGAGAC.GCTGCGCTCAGAGGAACAAGCCAGGCGTGTACACAAGGCTCCCTCTGTTTCGGGAATGGATCAAAG 2372

2574 AGAACACTGGGGTATAGGGGCCGGGGCCACCCAAATGTGTACACCTGCGGGGCCACCCATCGTCCACCCCAGTGTGCACGCCTGCAGGCTGGAGACT... 2670
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2373 AGAACACTGGGGTATAGGGGCCGGGGCCACCCAAATGTGTACACCTGCGGGGCCACCCATCGTCCACCCCAGTGTGCACGCCTGCAGGCTGGAGACTCGC 2472

2671 GGACCGCTGACTGCACCAGCGCCCCCAGAACATACACTGTGAACTCAATCTCCAGGGCTCCAAATCTGCCTAGAAAACCTCTCGCTTCCTCAGCCTCCAA 2770
     | ||||    |||||||||||| |||||||||||||||||||||||| ||||||||    |||||||| ||||||||||||||||||||||||||||||
2473 GCACCGTGACCTGCACCAGCG.CCCCAGAACATACACTGTGAACTC.ATCTCCAGG..CTCAAATCTG.CTAGAAAACCTCTCGCTTCCTCAGCCTCCAA 2567
```

Fig. 12D

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2771 AGTGGAGCTGGGA.GGTAGAAGGGGAGG.ACACTGGTGGTTCTACTGACCCAACTGGGGGCAAAGGTTTGAAGACACAGCCTCCCCCGCCAGCCCCAAGC 2868
     |||||||||||||| |||||||||||||| |||||||||||||||||||||||||||||||   |||||||||||| |||||    | ||| ||||||  |
2568 AGTGGAGCTGGGAGGGTAGAAGGGGAGGAACACTGGTGGTTCTACTGACCCAACTGGGG..CAAGGTTTGAAG.CACAG....CTCCGGCAGCCC..AAG 2658

2869 TGGGCCGAGGCGCGTTTGTGTATATCTGCCTCCCCTGTCTGTAAGGAGCAGCGGGAACGGAGCTTCGGAGCCTCCTCAGTGAAGGTGGTGGGGCTGCCGG 2968
     |||||   | |||||||||| ||| ||||| |  || | |  | |||  | | |||                ||  |||||     ||| | |||||||
2659 TGGGCGAGGACGCGTTTGTGCATA.CTGCC.CTGCTCTATACACGGAAGACCTGGA.................TCTCTAGTGA.....GTGTGACTGCCGG 2735

2969 ATCTGGGCTGTGGGGCCCTTGGGCCACGCTCTTGAGGAAGCCCAGGCTCGGAGGACCCTGGAAAACAGACGGGTCTGAGACTGAAATTGTTTTACCAGCT 3068
     ||||||    || || |||||| |     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| || ||||||||||
2736 ATCTGG...CTGTGGTCCTTGGCCACGCTTCTTGAGGAAGCCCAGGCTCGGAGGACCCTGGAAAACAGACGGGTCTGAGACTGAAAATGGTTTACCAGCT 2832

3069 CCCAGGGTGGACTTCAGTGTGTGTATTTGTGTAAATGGGTAAAACAATTTATTTCTTTTTAAAAAAAAAAAAAAAAAAA 3147 (SEQ ID NO: 1)
     ||||||   |||||||||||||||| |||||||||| |||||||| |||||||||||||||||||||||
2833 CCCAGG..TGACTTCAGTGTGTGTA.TTGTGTAAATGAGTAAAACATTTTATTTCTTTTTAAAAAAAAAAA..... 2900 (SEQ ID NO: 9)
```

Fig. 12E

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Fig. 10A

Fig. 10B

Fig. 10C

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Fig. 10D

Fig. 10E

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Fig. 10A

Fig. 10B

Fig. 10C

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Fig. 10D

Fig. 10E